Amendments to the Claims

This listing of claims will replace all prior versions and listings of claims in the application.

Listing of Claims

1-18 (Cancelled)

19. (Withdrawn) A gene signature predictive of patient response or outcome to anti-estrogen therapy for recurring breast cancer, comprising two or more marker genes identified in Table 1 as differentially expressed in primary tumors of recurring breast cancer patients exhibiting an outcome to anti-estrogen therapy with a significance of $p \leq 0.05$.

20. (Withdrawn) The gene signature of claim 19, wherein said marker genes are selected from the 81-gene signature listed in Table 1.

21. (Withdrawn) The gene signature of claim 19, wherein said marker genes are selected from the 44-gene signature listed in Table 1.

22. (Withdrawn) The gene signature of claim 19, wherein said marker genes comprise at least one of FN-1, CASP-2, THRAP-2, SIAH-2, DEME-6, TNC, and COX-6C.

23. (Withdrawn) The gene signature of claim 19, wherein said marker genes comprise at least one of TNC, SIAH-2, DEME-6, and COX-6C.

24. (Withdrawn) The gene signature of claim 19, wherein said marker genes comprise at least one of FN-1, CASP-2, THRAP-2, SIAH-2, and DEME-6.

25. (Withdrawn) The gene signature of claim 19, wherein said marker genes comprise at least one of CASP-2 and DEME-6, and at least one of SIAH-2 and TNC.

26. (Withdrawn) An assay system for predicting patient response or outcome to anti-estrogen therapy for recurring breast cancer configured and adapted to detect the gene signature of claim 19, comprising:

a) two or more marker genes identified in Table 1 as differentially expressed in primary tumors of recurring breast cancer patients exhibiting an outcome to anti-estrogen therapy with a significance of $p \leq 0.05$;

b) two or more nucleic acid probes, comprising at least 10 to 50 contiguous nucleic acids of marker genes identified in Table 1 as differentially expressed in primary tumors of recurring breast cancer patients exhibiting an outcome to anti-estrogen therapy with a significance of $p \leq 0.05$, or complementary nucleic acid sequences thereof; or

c) two or more binding ligands that specifically detect polypeptides encoded by marker genes identified in Table 1 as differentially expressed in primary tumors of recurring breast cancer patients exhibiting an outcome to anti-estrogen therapy with a significance of $p \leq 0.05$.

27. (Withdrawn) The assay system of claim 26, wherein said marker genes are selected from the 81-gene signature listed in Table 1.

28. (Withdrawn) The assay system of claim 26, wherein said marker genes are selected from the 44-gene signature listed in Table 1.

29. (Withdrawn) The assay system of claim 26, wherein said marker genes comprise at least one of FN-1, CASP-2, THRAP-2, SIAH-2, DEME-6, TNC, and COX-6C.

30. (Withdrawn) The assay system of claim 26, wherein said marker genes comprise at least one of TNC, SIAH-2, DEME-6, and COX-6C.

31. (Withdrawn) The assay system of claim 26, wherein said marker genes comprise at least one of FN-1, CASP-2, THRAP-2, SIAH-2, and DEME-6.

32. (Withdrawn) The assay system of claim 26, wherein said marker genes comprise at least one of CASP-2 and DEME-6, and at least one of SIAH-2 and TNC.

33. (Withdrawn) The assay system of claim 26, wherein said marker genes, nucleic acid probes, or binding ligands are disposed on an assay surface.

34. (Withdrawn) The assay system of claim 26, wherein said assay surface comprises a chip, array, or fluidity card.

35. (Withdrawn) The assay system of claim 26, wherein said probes comprise complementary nucleic acid sequences to at least 10 to 50 nucleic acid sequences of said marker genes.

36. (Withdrawn) The assay system of claim 26, wherein said binding ligands comprise antibodies or binding fragments thereof.

37. (Currently amended) A method for predicting outcome of anti-estrogen therapy for recurrent breast cancer, the method comprising:

a) analyzing a patient's primary tumor for expression of two or more marker genes identified in Table [[1]] 2 as differentially expressed in primary tumors of recurring breast cancer patients exhibiting an outcome to anti-estrogen therapy with a significance of $p \leq 0.05$, wherein said two or more marker genes comprise SIAH-2 and DEME-6;

b) determining if the expression pattern of said tumor's marker genes correlates with a Cluster 1 or Cluster 2 expression pattern, wherein a reduced expression of SIAH-2 and DEME-6 in said primary tumor, as compared to a reference sample, is indicative of a Cluster 1 expression pattern; and wherein elevated expression of SIAH-2 and DEME-6 in said primary tumor, as compared to a reference sample, is indicative of a Cluster 2 expression pattern; and

c) predicting outcome of anti-estrogen therapy for recurrent breast cancer as Progressive Disease if the expression pattern is indicative of ~~correlating~~ a Cluster 1 expression pattern and predicting outcome of anti-estrogen therapy as Objective

Response if the expression pattern is indicative of ~~with prediction of Progressive Disease and~~ a Cluster 2 expression pattern ~~with Objective Response to anti-estrogen therapy for recurrent breast cancer~~.

38. (Withdrawn and currently amended) The method of claim 37, wherein said primary tumor is analyzed for expression of the 81-gene signature or the 44-gene ~~signaure~~ signature listed in Table [[1]] 2.

39. (Currently amended) A method for predicting Progression Free Survival of anti-estrogen therapy for recurrent breast cancer, the method comprising:

a) analyzing a patient's primary tumor for expression of two or more marker genes identified in Table [[1]] 2 as differentially expressed in primary tumors of recurring breast cancer patients exhibiting an outcome to anti-estrogen therapy with a significance of $p \leq 0.05$, wherein said two or more marker genes comprise SIAH-2 and DEME-6;

b) determining if the expression pattern of said tumor's marker genes correlates with a Cluster 1 or Cluster 2 expression pattern, wherein a reduced expression of SIAH-2 and DEME-6 in said primary tumor, as compared to a reference sample, is indicative of a Cluster 1 expression pattern; and wherein elevated expression of SIAH-2 and DEME-6 in said primary tumor, as compared to a reference sample, is indicative of a Cluster 2 expression pattern; and

c) negatively predicting Progression Free Survival of anti-estrogen therapy for recurrent breast cancer if the expression pattern is indicative of a Cluster 1 expression pattern, and positively predicting Progression Free Survival if the expression pattern is indicative of a Cluster 2 expression pattern~~correlating a Cluster 1 expression pattern with a negative prediction of Progression Free Survival for recurrent breast cancer and a Cluster 2 expression pattern with a positive Progression Free Survival for recurrent breast cancer~~.

40. (Withdrawn and Currently amended) The method of claim 39, wherein said primary tumor is analyzed for expression of the [[the]] 81-gene signature or the 44-gene ~~signaure~~ signature listed in Table [[1]] 2.

41. (New) The method according to claim 37, wherein said reference sample comprises a cell line pool of cell lines from different tissue origins.

42. (New) The method according to claim 39, wherein said reference sample comprises a cell line pool of cell lines from different tissue origins.